

~~ATC~~

01/01/01
O/PE

CRF Errors Corrected by the STIC Systems Branch

CRF Processing Date:

Edited by:

Verified by:

Serial Number: 09/836,544

ENTERED

12/7/2001

(STIC stat)

Changed a file from non-ASCII to ASCII

Changed the margins in cases where the sequence text was 'wrapped' down to the next line

Edited a format error in the Current Application Data section, specifically:

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MAR 01 2002
OFFICE OF PETITIONS

Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other _____

Added the mandatory heading and subheadings for 'Current Application Data'.

Edited the 'Number of Sequences' field. The applicant spelled out a number instead of using an integer.

Changed the spelling of a mandatory field (the headings or subheadings), specifically:

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

Inserted colons after headings/subheadings. Headings edited included: _____

Deleted extra/invalid, headings used by an applicant, specifically:

Deleted: non-ASCII 'garbage' at the beginning/end of files; secretary initials/filename at end of file;
 page numbers throughout text; other invalid text, such as _____

Inserted mandatory headings, specifically: _____

Corrected an obvious error in the response, specifically:

Edited identifiers where upper case is used but lower case is required, or vice versa.

Corrected an error in the Number of Sequences field, specifically:

A 'Hard Page Break' code was inserted by the applicant. All occurrences had to be deleted.

Deleted ending stop codon in amino acid sequences and adjusted the '(A)Length:' field accordingly (error due to a PatentIn bug). Sequences corrected: _____

Other:

Examiner: The above corrections must be communicated to the applicant in the first Office
Action! DO NOT send a copy of this form.

3/1/95

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/836,544

DATE: 12/07/2001
TIME: 19:09:11

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\12072001\I836544.raw

3 <110> APPLICANT: The General Hospital Corporation
 5 <120> TITLE OF INVENTION: Rapid Immunoselection Cloning Method
 7 <130> FILE REFERENCE: 11-88L
 9 <140> CURRENT APPLICATION NUMBER: US 09/836,544
 10 <141> CURRENT FILING DATE: 2001-04-17
 12 <150> PRIOR APPLICATION NUMBER: US 07/983,647
 13 <151> PRIOR FILING DATE: 1992-12-01
 15 <150> PRIOR APPLICATION NUMBER: US 07/553,759
 16 <151> PRIOR FILING DATE: 1990-07-13
 18 <150> PRIOR APPLICATION NUMBER: US 07/498,809
 19 <151> PRIOR FILING DATE: 1990-03-23
 21 <150> PRIOR APPLICATION NUMBER: US 07/379,076
 22 <151> PRIOR FILING DATE: 1989-07-13
 24 <150> PRIOR APPLICATION NUMBER: US 07/160,416
 25 <151> PRIOR FILING DATE: 1988-02-25
 27 <160> NUMBER OF SEQ ID NOS: 37
 29 <170> SOFTWARE: PatentIn Ver. 2.0
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 2932
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Artificial Sequence
 36 <220> FEATURE:
 37 <223> OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
 sequence of expression vector, piH3
 40 <400> SEQUENCE: 1
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 43 gatcaagagc taccacttct ttttccgaag gaactggctt cagcagagcg cagataccaa 120
 45 atactgtcct tcttagttagt ccgttagttt gcccaccatt caagaactct gtacgaccgc 180
 47 ctacatactt cgctctgtca atcctgttac cagtggctgc tgccagtggc gataagtctgt 240
 49 gtcttacggg gttggactca agacgatagt taccggataa ggccgcaggcc tcgggctgaa 300
 51 cggggggtttc gtgcacacag cccagcttgg agcgaacgac ctacaccgaa ctgagataacc 360
 53 tacagcgta gctatgagaa agcgcacgc ttcccaagg gagaaggcc gacaggtatc 420
 55 cggtaagccg cagggtcgga acaggagagc gcacaggccg gcttccaggg gaaacgcct 480
 57 ggtatctta tagtccgtc gggtttcggcc acctctgact tgagcgtcga ttttgtat 540
 59 gctcgctagg gggcgccggc ctatggaaaa acgcccacaa cggccgatata ccgcgggttt 600
 61 totcaacgtt acactttaca gggcgccgtc atttgatatg atgcgcggcc cttcccgata 660
 63 agggagcagg ccagtaaaag cattaccgtt ggtgggggtt ccgagcggcc aaaggagca 720
 65 gactctaattt ctgcgtcat cgacttcgaa ggttcaatc cttccccac caccatca 780
 67 ttcaaaaatc cgaagaatc tgctccgtc ttgtgtgtt gaggtcgctg agtagtgcgc 840
 69 gagtaaaatt taagctacaa caaggcaagg cttgaccgac aattgtatc agaatctgtt 900
 71 tagggtttagg cgtttcgcc tgcttcgca tgtaaaaaatc agatatacgc gttgacattt 960
 73 attattgact agttatataat agtaatcaat tacggggta ttatgttataa gccatatat 1020
 75 ggagttccgc gttacataac ttacggtaaa tggccgcct ggctgaccgc ccaacgaccc 1080
 77 ccccccattt acgtcaataa tgacgtatgt tcccatatgt acgccaatag ggactttcca 1140
 79 ttgacgtcaa tgggtggact atttacggta aactgcccac ttggcagtttac atcaagtgtt 1200
 81 tcatatgcca agtacgcccc cttatgacgtt caatgacggt aaatggcccg cctggcatta 1260
 83 tgcccaatc atgaccttat gggactttcc tacttggcag tacatctacg tattatgtat 1320

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87	ctcacggga	tttccaagtc	tccaccccat	tgacgtcaat	gggagtttg	tttggcacca	1440
89	aaatcaacgg	gactttccaa	aatgtcgtaa	caactccgccc	ccattgacgc	aatgggcgg	1500
91	aattcctggg	cgggactggg	gagtggcgg	ccctcagatg	ctgcatataa	gcagctgtt	1560
93	tttgcctgta	ctgggtctct	ctggttagac	cagatctgag	cctgggagct	ctctggctaa	1620
95	ctagagaacc	cactgcttaa	gcctcaataa	agcttctaga	gatccctcga	cctcgaggga	1680
97	tottccatac	ctaccaggtc	tgccctgca	ggtcgggccc	gcgactctag	aggatcttg	1740
99	tgaaggaacc	ttacttcgt	ggtgtgacat	aattggacaa	actacctaca	gagatttaaa	1800
101	gctctaagg	aaatataaaa	ttttaagt	tataatgtgt	taaactactg	attctaattt	1860
103	tttgtgtatt	tttagattcca	acctatggaa	ctgatgaatg	ggagcagtgg	tggaatgcct	1920
105	ttaatgagga	aaacctgttt	tgctcagaag	aaatgccatc	tagtgtatgt	gaggctactg	1980
107	ctgactctca	acattctact	cctccaaaaaa	agaagagaaa	ggtagaaagac	cccaaggact	2040
109	ttccttcaga	attgctaagt	tttttgagtc	atgctgtgtt	tagtaataga	actcttgctt	2100
111	gcttgctat	ttacaccaca	aaggaaaaag	ctgcactgct	atacaagaaa	attatggaaa	2160
113	aatattctgt	aaccttata	agtaggcata	acagtataa	tcataacata	ctgtttttc	2220
115	ttactccaca	caggcataga	gtgtctgcta	ttaataacta	tgctcaaaaa	tttgttacct	2280
117	ttagctttt	aatttgaaa	ggggtaata	aggaatattt	gatgtatagt	gccttgacta	2340
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121	cacccccc	tgaacctgaa	acataaaaatg	aatgcaattt	ttttgtttaa	cttggtttatt	2460
123	gcagcttata	atggtacaa	ataaagcaat	agcatcacaa	atttcacaaa	taaagcattt	2520
125	tttctactgc	attctagtt	ttgtttgtcc	aaactctatca	atgttatctt	tcatgtctgg	2580
127	atccctgtgg	atgtgtgtca	gttaggggt	ggaaagtccc	caggctcccc	agcaggcaga	2640
129	agtatgcaaa	gcatgcatct	caattgtca	gcaaccagg	gtggaaagt	cccaggctcc	2700
131	ccagcaggca	gaagtatgca	aagcatgcat	ctcaattgt	cagcaaccat	agtcccggcc	2760
133	ctaactccgc	ccatcccgcc	cctaactcg	cccagttccg	ccattctcc	gccccatggc	2820
135	tgactaattt	tttttattta	tgccagaggcc	gagggccct	gggcctctga	gttattccag	2880
137	aagtaqttag	gaggctttt	tgaggcccta	ggcttttgca	aaaagctaat	tc	2932

140 <210> SEQ ID NO: 2

141 <211> LENGTH: 1504

142 <212> TYPE: DNA

143 <213> ORGANISM: *Homo sapiens*

143 <213> ORGANISM
145 <220> FEATURE

145 <220> FEATURE.

146 <221> NAME/REF: CDS
147 000: LOCATION: (7) (1059)

147 <222> LOCATION: (148-149) SEQUENCE: 3

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149 <400> SEQUENCE: 2 48
150 cctaag atg agc ttt cca tgt aaa ttt gta gcc agc ttc ctt ctg att
151 Met Ser Phe Pro Cys Lys Phe Val Ala Ser Phe Leu Leu Ile
152 1 5 10 96
154 ttc aat gtt tct tcc aaa ggt gca gtc tcc aaa gag att acg aat gcc
155 Phe Asn Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala
156 15 20 25 30 144
158 ttg gaa acc tgg ggt gcc ttg ggt cag gac atc aac ttg gac att cct
159 Leu Glu Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro
160 35 40 45 192
162 agt ttt caa atg agt gat att gac gat ata aaa tgg gaa aaa act
163 Ser Phe Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr
164 50 55 60 240
166 tca gac aag aaa aag att gca caa ttc aga aaa gag aaa gag act ttc
167 Ser Asp Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe

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Output Set: N:\CRF3\12072001\I836544.raw

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170	aag gaa aaa gat aca tat aag cta ttt aaa aat gga act ctg aaa att				
171	Lys Glu Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile				
172	80	85	90		336
174	aag cat ctg aag acc gat gat cag gat atc tac aag gta tca ata tat				
175	Lys His Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr				
176	95	100	105		384
178	gat aca aaa gga aaa aat gtg ttg gaa aaa ata ttt gat ttg aag att				
179	Asp Thr Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile				
180	115	120	125		432
182	caa gag agg gtc tca aaa cca aag atc tcc tgg act tgt atc aac aca				
183	Gln Glu Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr				
184	130	135	140		480
186	acc ctg acc tgt gag gta atg aat gga act gac ccc gaa tta aac ctg				
187	Thr Leu Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu				
188	145	150	155		528
190	tat caa gat ggg aaa cat cta aaa ctt tct cag agg gtc atc aca cac				
191	Tyr Gln Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His				
192	160	165	170		576
194	aag tgg acc acc agc ctg agt gca aaa ttc aag tgc aca gca ggg aac				
195	Lys Trp Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn				
196	175	180	185		624
198	aaa gtc agc aag gaa tcc agt gtc gag cct gtc agc tgt cca gag aaa				
199	Lys Val Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys				
200	195	200	205		672
202	ggt ctg gac atc tat ctc atc att ggc ata tgt gga gga ggc agc ctc				
203	Gly Leu Asp Ile Tyr Leu Ile Gly Ile Cys Gly Gly Ser Leu				
204	210	215	220		720
206	ttg atg gtc ttt gtg gca ctg ctc gtt ttc tat atc acc aaa agg aaa				
207	Leu Met Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys				
208	225	230	235		768
210	aaa cag agg agt cgg aga aat gat gag gag ctg gag aca aga gcc cac				
211	Lys Gln Arg Ser Arg Arg Asn Asp Glu Leu Glu Thr Arg Ala His				
212	240	245	250		816
214	aga gta gct act gaa gaa agg ggc cgg aag ccc cac caa att cca gct				
215	Arg Val Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala				
216	255	260	265		864
218	tca acc cct cag aat cca gca act tcc caa cat cct cct cca cca cct				
219	Ser Thr Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Pro				
220	275	280	285		912
222	ggt cat cgt tcc cag gca cct agt cat cgt ccc ccg cct cct gga cac				
223	Gly His Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His				
224	290	295	300		960
226	cgt gtt cag cac cag cct cag aag agg cct cct gct ccg tcg ggc aca				
227	Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr				
228	305	310	315		1008
230	caa gtt cac cag cag aaa ggc ccg ccc ctc ccc aga cct cga gtt cag				
231	Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln				
232	320	325	330		

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234 cca aaa cct ccc cat ggg gca gca gaa aac tca ttg tcc cct tcc tct 1056
 235 Pro Lys Pro Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser 350
 236 335 340 345 350
 238 aat taaaaaagat agaaaactgtc ttttcaata aaaagcactg tggatttctg 1109
 239 Asn
 241 ccctcctgat gtgcataatcc gtacttccat gaggtgtttt ctgtgtgcag aacattgtca 1169
 243 cctcctgagg ctgtggcca cagccaccc tcgcatttcg aactcagcca tgggtcaac 1229
 245 atctggagtt ttgggtctcc tcagagagct ccatcacacc agtaaggaga agcaatataa 1289
 247 gtgtgattgc aagaatggta gaggaccgag cacagaaatc ttagagattt cttgtcccct 1349
 249 ctcaggtcat gtgttagatgc gataaatcaa gtgattgtg tgcctgggtc tcactacaag 1409
 251 cagcctatct gcttaagaga ctctggagtt tcttatgtgc cctgggtggac acttgcccac 1469
 253 catcctgtga gtaaaaagtga aataaaaagct ttgac 1504
 256 <210> SEQ ID NO: 3
 257 <211> LENGTH: 351
 258 <212> TYPE: PRT
 259 <213> ORGANISM: Homo sapiens
 261 <400> SEQUENCE: 3
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 265 20 25 30
 266 Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro Ser Phe
 267 35 40 45
 268 Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp
 269 50 55 60
 270 Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu
 271 65 70 75 80
 272 Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile Lys His
 273 85 90 95
 274 Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr
 275 100 105 110
 276 Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu
 277 115 120 125
 278 Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu
 279 130 135 140
 280 Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln
 281 145 150 155 160
 282 Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp
 283 165 170 175
 284 Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val
 285 180 185 190
 286 Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu
 287 195 200 205
 288 Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Ser Leu Leu Met
 289 210 215 220
 290 Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys Lys Gln
 291 225 230 235 240
 292 Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His Arg Val
 293 245 250 255
 294

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Input Set : A:\PTO.AMC.txt
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310 Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala Ser Thr
311 260 265 270
313 Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Pro Gly His
314 275 280 285
316 Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His Arg Val
317 290 295 300
319 Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val
320 305 310 315 320
322 His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln Pro Lys
323 325 330 335
325 Pro Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser Asn
326 340 345 350
329 <210> SEQ ID NO: 4
330 <211> LENGTH: 874
331 <212> TYPE: DNA
332 <213> ORGANISM: Homo sapiens
334 <220> FEATURE:
335 <221> NAME/KEY: CDS
336 <222> LOCATION: (13)..(723)
338 <400> SEQUENCE: 4
339 gccccgacgag cc atg gtt gct ggg agc gac gcg ggg gcc ctg ggg gtc 51
340 Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val 10
341 1 5 10
343 ctc agc gtg gtc tgc ctg ctg cac tgc ttt ggt ttc atc agc tgt ttt 99
344 Leu Ser Val Val Cys Leu Leu His Cys Phe Gly Ile Ser Cys Phe
345 15 20 25
347 tcc caa caa ata tat ggt gtt gtg tat ggg aat gta act ttc cat gta
348 Ser Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val
349 30 35 40 45
351 cca agc aat gtg cct tta aaa gag gtc cta tgg aaa aaa caa aag gat 195
352 Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp
353 50 55 60
355 aaa gtt gca gaa ctg gaa aat tct gaa ttc aga gct ttc tca tct ttt 243
356 Lys Val Ala Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe
357 65 70 75
359 aaa aat agg gtt tat tta gac act gtg tca ggt agc ctc act atc tac 291
360 Lys Asn Arg Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr
361 80 85 90
363 aac tta aca tca tca gat gaa gat gag tat gaa atg gaa tcg cca aat 339
364 Asn Leu Thr Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn
365 95 100 105
367 att act gat acc atg aag ttc ttt ctt tat gtg ctt gag tct ctt cca 387
368 Ile Thr Asp Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro
369 110 115 120 125
371 tot ccc aca cta act tgt gca ttg act aat gga agc att gaa gtc caa 435
372 Ser Pro Thr Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln
373 130 135 140
375 tgc atg ata cca gag cat tac aac agc cat cga gga ctt ata atg tac 483
376 Cys Met Ile Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/836,544

DATE: 12/07/2001
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